

## Sequence ID No. 4

CGGGAGAATAGTGCACCAAGGGGATGCCCCGTGAAATATTAATTAAACGTTTTTTAAGAACA	-101
TCATCAAACCCGGGCCCCATCATGAAGGAATAACAAGGCCTTCGAAAAGTATGGGAAACT	-41
GGTCGGCAGGACATCAGCATTATTAATTCTAGGAAACTCATTATGGATAACAAGGAAACT	18
M D N K E T	6
AACGGAGAGCTAGAGCAGTCTGATGAGGCCGATCCGTCCGGTCAAACCTTGATGATGGG	78
N G E L E Q S D E A D P S G Q N L D D G	26
GAAACCGATAGCAAACAAGAAGAGAATCTCATCAACGTTAGCCCGCCAAAAACACCGCCA	138
E T D S K Q E E N L I N V S P P K T P P	45
GGTCCTCCTCCTCCTCTAAAGAATGGAGGAAGGGGTCAGAAACCGCCCCAAAATCCCAATA	198
G P P P P L K N G G R G Q K P P K I P I	66
TGTCATCAAATGGAAAGCTCCCCAAGGAAGTTGAATGGACAGAAGACAGAGGCGAAGAC	258
C H Q N G K L P K E V E W T E D R G E D	86
AGAAAGGATAGTCTCACTCTTCAATCAAAGCTAGATCACGGGGCATACACGGATGAGAAA	318
R K D S L T L Q S K L D H G A Y T D E K	106
CAGGATCTTCTAACATATCTTGACCGTCACGGCATCAACAGTCCAGTCAAGCTAACACCA	378
Q D L L T Y L D R H G I N S P V K L T P	126
GATGAAACTGGAGGGAGCAGTGCTTTGGATATTCTTGGGATTATTGAAGAGAGGGACACT	438
D E T G G S S A L D I L G I I E E R D T	146
GGTGCACCTAGGCTCTGATCCCTCATCCACTATGCAGGCCATGGCTAAACCTGTAGGCTTT	498
G A L G S D P S S T M Q A M A K P V G F	166
CTGCAGAGGCAGCTATGGACTGTCCTCCAACCTTCAGACAATAGACTCTCCATGAAACTT	558
L Q R Q L W T V L Q P S D N R L S M K L	186
TTCCGAAGCAAGAAAGGGTTACAAAAGGAAAAATATCGGCTGAGGAAGGCGGGGGTTCTT	618
F G S K K G L Q K E K Y R L R K A G V L	206
S1	
ATCATTTCATCCATGTAGTCATTTTCAGATTTTACTGGGATCTACTGATGCTGTGCCTGATC	678
I I H P C S H F R F Y W D L L M L C L I	226
ATGGCAAACGTCATCCTCCTACCCGTCGTCATTACTTTCTTCCACAACAAGGACATGAGT	738
M A N V I L L P V V I T F F H N K D M S	246
S2	
ACGGGTTGGCTCATCTTTAATTGCTTCTCAGATACCTTCTTCATTCTCGATCTCATCTGC	798
T G W L I F N C F S D T F F I L D L I C	266
AACTTTTCGGACCGGCATCATGAATCCGAAGTCGGCCGAACAGGTGATCCTCAACCCCGT	858
N F R T G I M N P K S A E Q V I L N P R	286
S3	
CAAATCGCCTATCATTATCTCCGTTTCATGGTTTCATCATCGATCTCGTGTCTTCCATCCC	918
Q I A Y H Y L R S W F I I D L V S S I P	306

ATGGACTACATCTTCCTCCTCGCTGGCGGCCAGAACCGTCACTTCCTCGAGGTGTCCCGA 978  
M D Y I F L L A G G Q N R H F L E V S R 326

## S4

GCCCTCAAGATACTGCGCTTTGCCAAGCTCCTCAGTCTTCTTCGACTCCTGCGTCTGTCC 1038  
A L K I L R F A K L L S L L R L L R L S 346

AGGCTCATGCGGTTCGTCACTCAATGGGAACAGGCCTTCAACGTAGCCAATGCCGTCATC 1098  
R L M R F V S Q W E Q A F N V A N A V I 366

## S5

CGGATCTGTAATCTAGTGTGTATGATGCTTCTGATTGGCCATTGGAATGGCTGCCTTCAA 1158  
R I C N L V C M M L L I G H W N G C L Q 386

TATCTCGTGCCCATGCTGCAAGAATACCCCGACCAATCATGGGTGCGCCATTAATGGCCTT 1218  
Y L V P M L Q E Y P D Q S W V A I N G L 406

## Pore

GAGCACGCTCATTGGTGGGAGCAGTATACATGGGCACTCTTCAAAGCCCTTTCGCACATG 1278  
E H A H W W E Q Y T W A L F K A L S H M 426

CTCTGTATCGGGTACGGCAAGTTCCCCCCTCAAAGCATCACCGATGTCTGGCTAACGATT 1338  
L C I G Y G K F P P Q S I T D V W L T I 446

## S6

GTCAGTATGGTGTCCGGTGCACCTGCTTCGCCCTGTTTCATCGGACACGCTACCAATCTC 1398  
V S M V S G A T C F A L F I G H A T N L 466

ATCCAGTCCATGGACTCCTCCAGCAGGCAATACCGTGAGAAGTTGAAACAAGTTGAAGAG 1458  
I Q S M D S S S R Q Y R E K L K Q V E E 486

TACATGCAGTATCGCAAGCTACCGTCCCACCTACGAAACAAGATCCTCGATTACTACGAG 1518  
Y M Q Y R K L P S H L R N K I L D Y Y E 506

TACCGATACCGAGGAAAGATGTTTGATGAGAGGCATATCTTTTCGAGAAGTGTCGGAGAGT 1578  
Y R Y R G K M F D E R H I F R E V S E S 526

ATACGACAGGATGTCGCAAACTACAATTGTCGCGACCTGGTTCGCATCCGTCCCTTTCTTC 1638  
I R Q D V A N Y N C R D L V A S V P F F 546

GTCGGTGCCGACTCAAACCTTCGTACCCCGTGTGGTGACGCTGCTCGAATTCGAGGTCTTC 1698  
V G A D S N F V T R V V T L L E F E V F 566

CAACCCGCTGACTATGTTATACAGGAAGGTACTTTTCGGTGATCGCATGTTCTTCATCCAG 1758  
Q P A D Y V I Q E G T F G D R M F F I Q 586

CAGGGCATCGTCGACATCATCATGTCCGACGGCGTCATCGCCACGTCAGTGACGGC 1818  
Q G I V D I I M S D G V I A T S L S D G 606

## cNMP binding site

TCATATTTTGGCGAAATCTGCCTGCTTACCCGTGAGCGCCGCGTGGCATCGGTGAAGTGC 1878  
S Y F G E I C L L T R E R R V A S V K C 626

GAGACCTACTGCACGCTCTTCTCGCTCTCCGTCCAGCATTTCAACCAAGTGCTCGACGAG 1938  
E T Y C T L F S L S V Q H F N Q V L D E 646

005640582 081700

TTTCCCGCCATGAGGAAAACGATGGAAGAGATAGCCGTTTCGTCTGACCCGAATCGGG	1998
F P A M R K T M E E I A V R R L T R I G	666
AAGGAATCGAGCAAGCTGAAATCCCGCCTAGAGAGCCCGACGATCAGGGACACTGCCCCCT	2058
K E S S K L K S R L E S P T I R D T A P	686
CTCTTTCCGATCCACCTGATACACCGTCTTTCGTACCCGACATCGAAAAGAACCGGTTC	2118
L F P I P P D T P S F V T D I E K N R F	706
TTTGGCGACGACACGGACGATGTACACATCAGGACCCGAGTCGACGTCGAGCGTGGTTCC	2178
F G D D T D D V H I R T R V D V E R G S	726
CATGAAAACGTCATCGCCATCATGGATGGGAGTTTATCCGACCTCAGGATGGAAAACGAA	2238
H E N V I A I M D G S L S D L R M E N E	746
ATCCAAGCCCGTAAATCGTCTAGCGGAAAACGGAGGAAATTCCAGCAACAAACAACCGAA	2298
I Q A R K S S S G K R R K F Q Q Q T T E	766
CTATGACGACTTGAAAACAAACAATGATGGACGCTTACAATTTCCAGTGATTCAATACTTA	2358
L -	767
CGCAATGCAGACATTAGCTTTTGTACCTGATTGTTTAGAATGTATTGAATTTGTAGATCA	2418
GTCCGGCAAATAAGAAAGCATAATTTGGAATTTCTTTCATTGAGGAAGTACTGAAAACAA	2478
TGTGATAGCAGCCGGTAGAAATTTCTTGTCCATTATCGAGGCTATATTTTTCGCGCTTTC	2538
TTACGAAGTAAATGAAAGGATCAATTAATTTATTGTTCTTTGTCTCGTGCCTTTGTATC	2598
TGATGCCGAAAAGGAATGAAACGTGATTAGAACAGTAATCGATTGAACTACAGAAGTCTT	2658
TTCAAAATGTTGAATGTATGAAGGAGGAGGGGGAAGGTTTGATATATGCAAAGAAATGGA	2718
GAAATATTTTTGTAAATTTATCTAGAATGGTACTATTGATGCTCGAAAGGTGTTGAAGTT	2778
GTCCAATATTGTGTCAAATCACCAACTATTTGACATTTGTCTTTTTC	2825

007180 28504960

Fig. 1B, 1C

B		S4 motif										C										pore																														
SPIH	326-	R	A	L	K	I	L	R	F	A	K	L	L	S	L	L	R	L	S	R	L	M	R	-350	416-	T	W	A	L	F	K	A	L	S	H	M	L	C	I	G	Y	G	K	F	P	P	Q	S	-438			
Shaker	344-	M	S	L	A	I	L	R	V	I	R	L	V	R	V	F	R	I	F	K	L	S	R	H	S	K	-368	418-	P	D	A	F	W	A	V	T	M	T	T	V	G	Y	G	D	M	T	P	V	G	-440		
DmEAG	341-	S	L	F	S	A	L	K	V	V	R	L	L	R	L	G	R	V	V	R	K	L	D	R	Y	L	-365	441-	V	T	A	L	V	F	T	M	T	C	M	T	S	V	G	F	G	N	V	A	A	E	T	-463
HERG	519-	E	L	I	G	L	L	K	T	A	R	L	L	R	L	V	R	V	A	R	K	L	D	R	Y	S	-343	612-	V	T	A	L	V	F	T	F	S	S	L	T	S	V	G	F	G	N	V	S	P	N	T	-634
KAT I	168-	S	M	L	R	L	W	R	L	R	R	V	S	S	L	F	A	R	L	E	K	D	I	R	F	N	-192	248-	V	T	A	L	V	W	S	T	T	T	T	T	T	G	Y	G	D	F	H	A	E	N	-270	
brCNGC $\alpha$	263-	W	N	Y	P	E	I	R	L	N	R	L	L	R	I	S	R	M	F	E	F	F	Q	R	T	E	-287	348-	V	Y	S	L	Y	W	S	T	L	T	L	T	T	I	G	-	E	T	P	P	P	V	-368	

**cNMP binding domain**

Fig. 1D

[illegible][illegible]

Fig. 2A, 2B

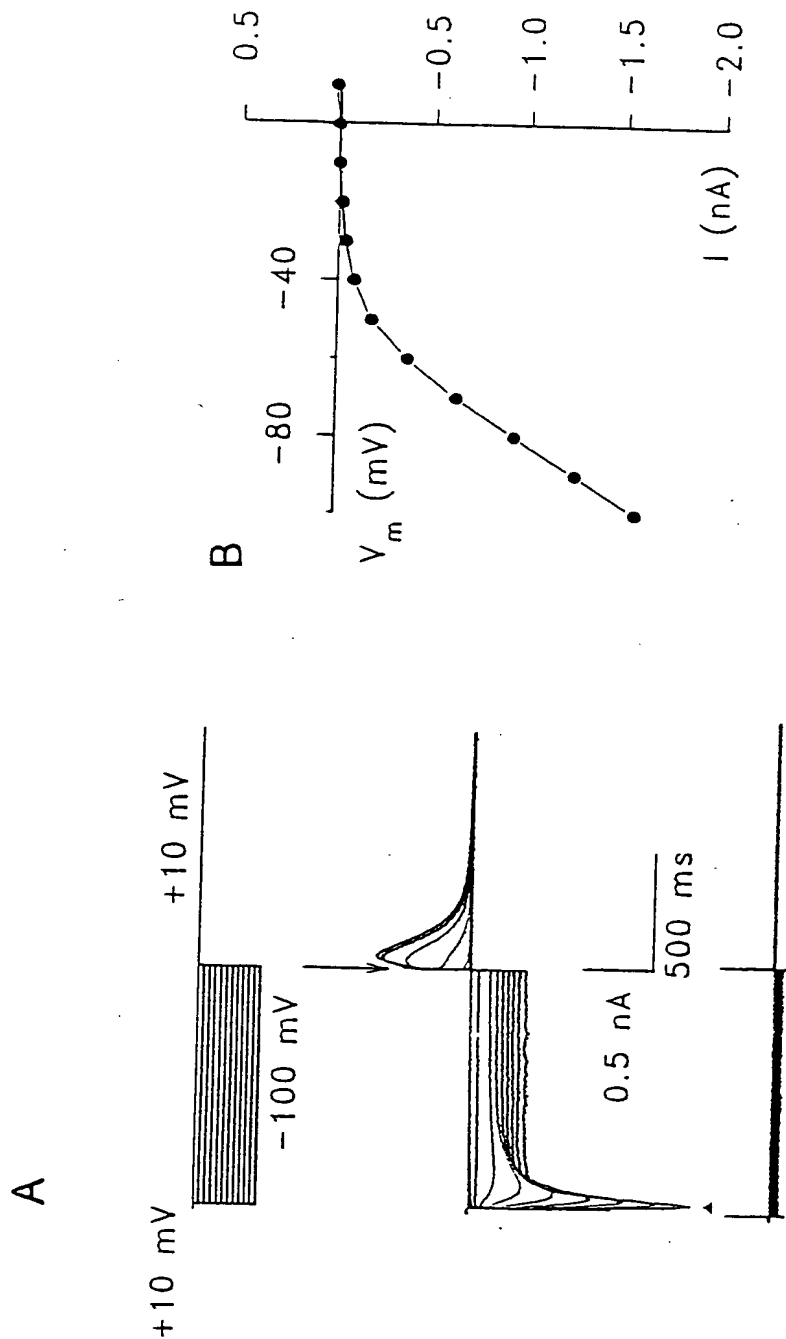
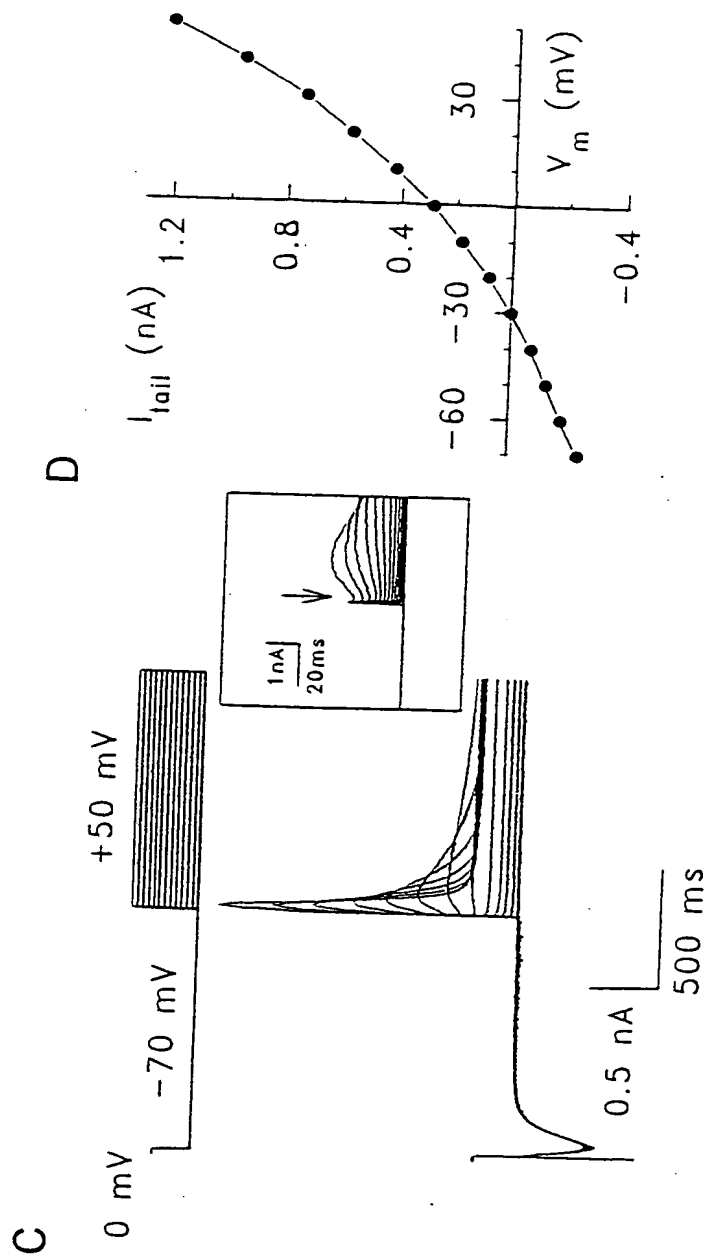


Fig. 2C, 2D



Fig, 2E, 2F

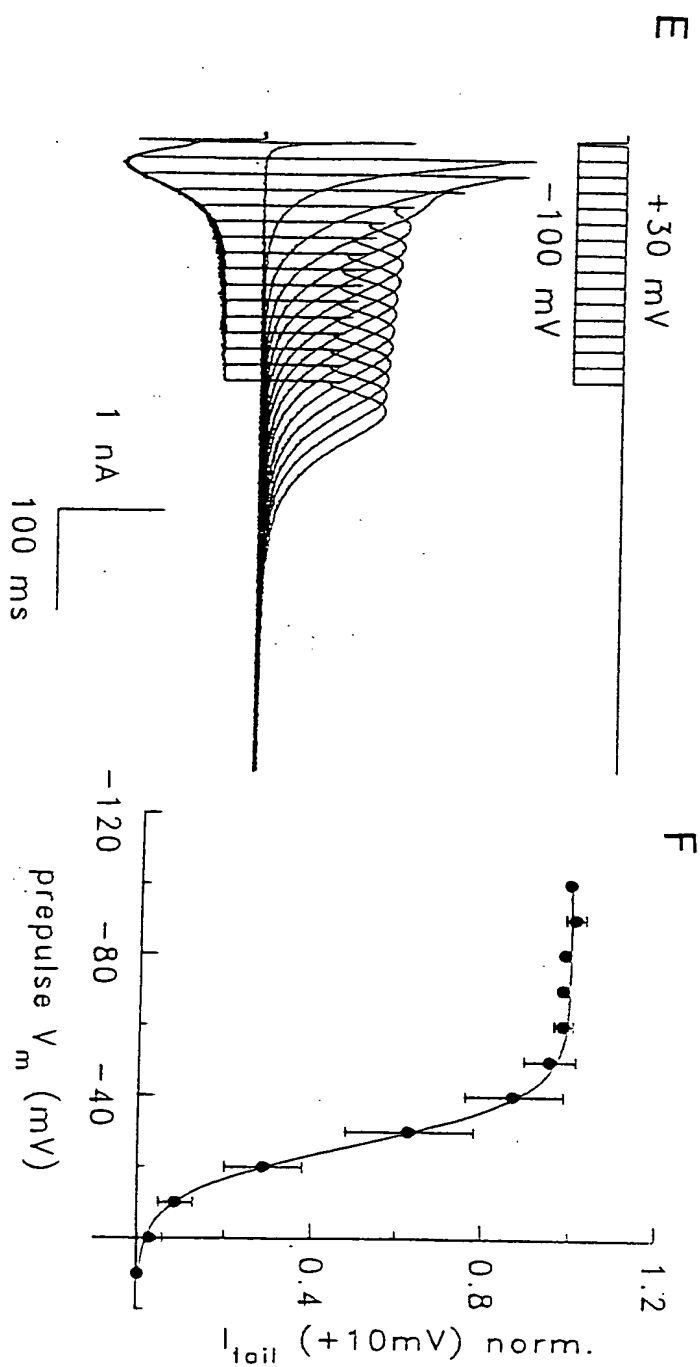




Fig. 3A, 3B

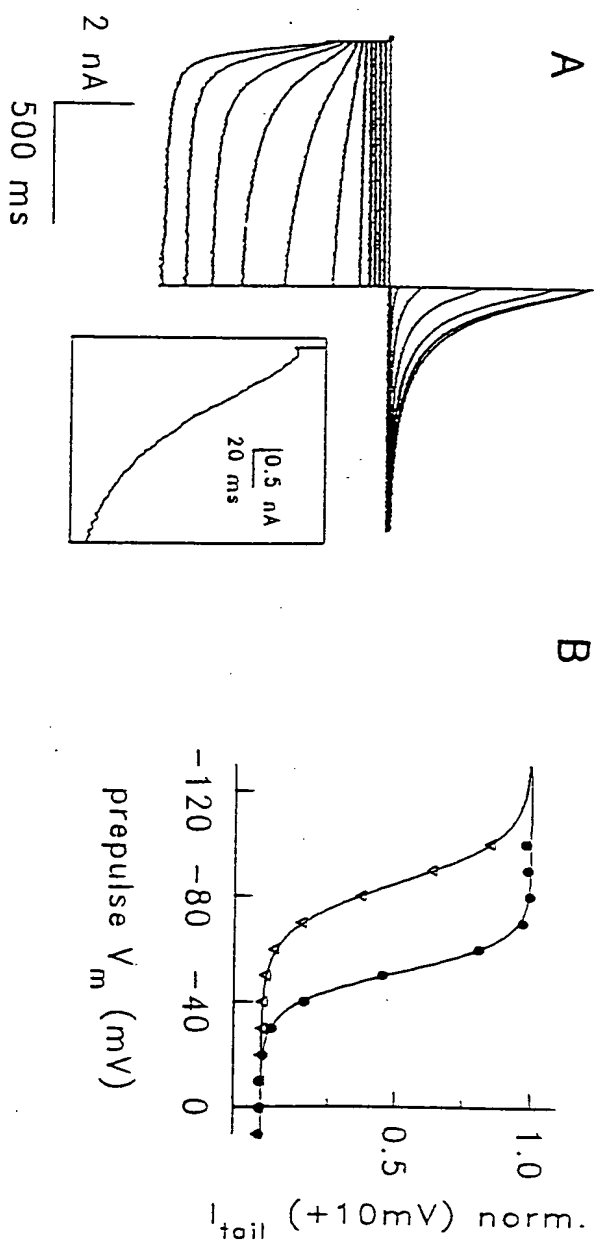


Fig. 3C, 3D

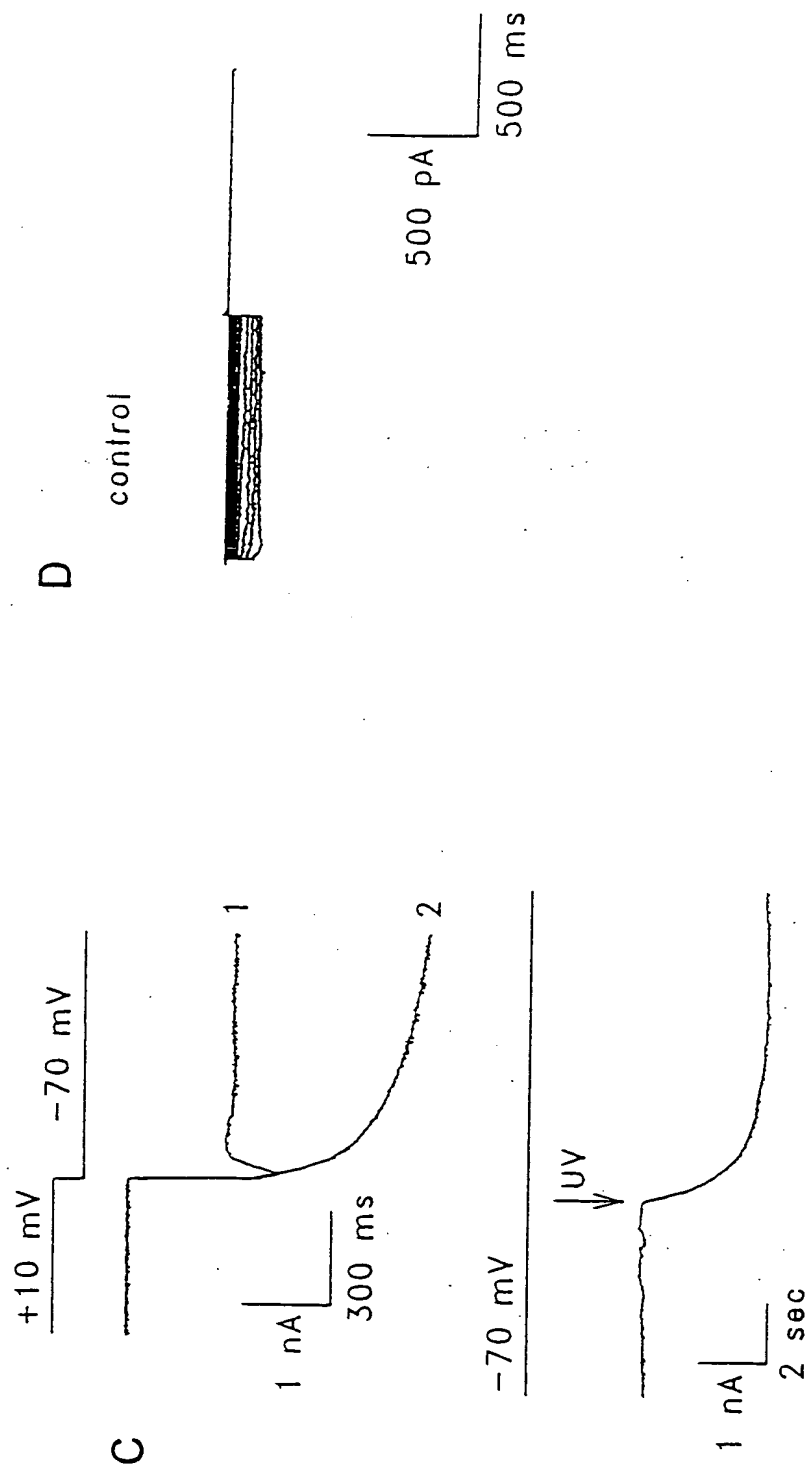
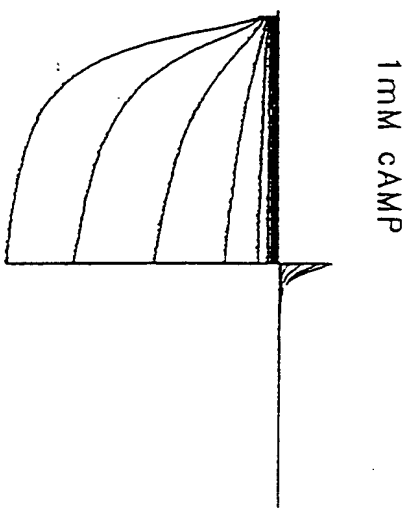


Fig. 3E, 3F

E



F

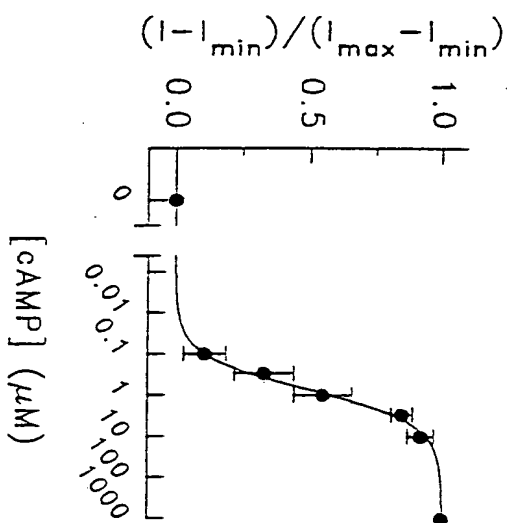


Fig. 4

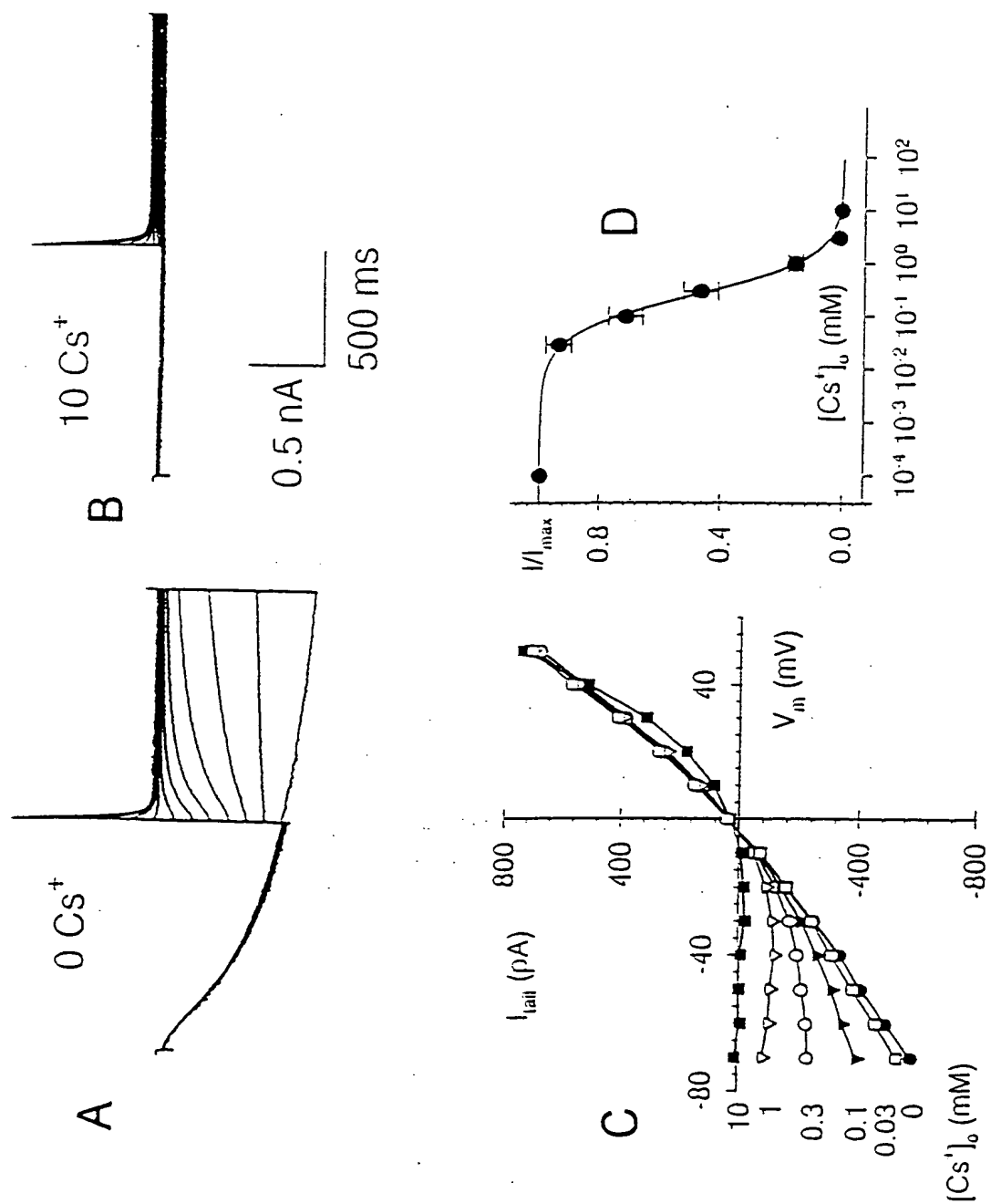


Fig. 4E

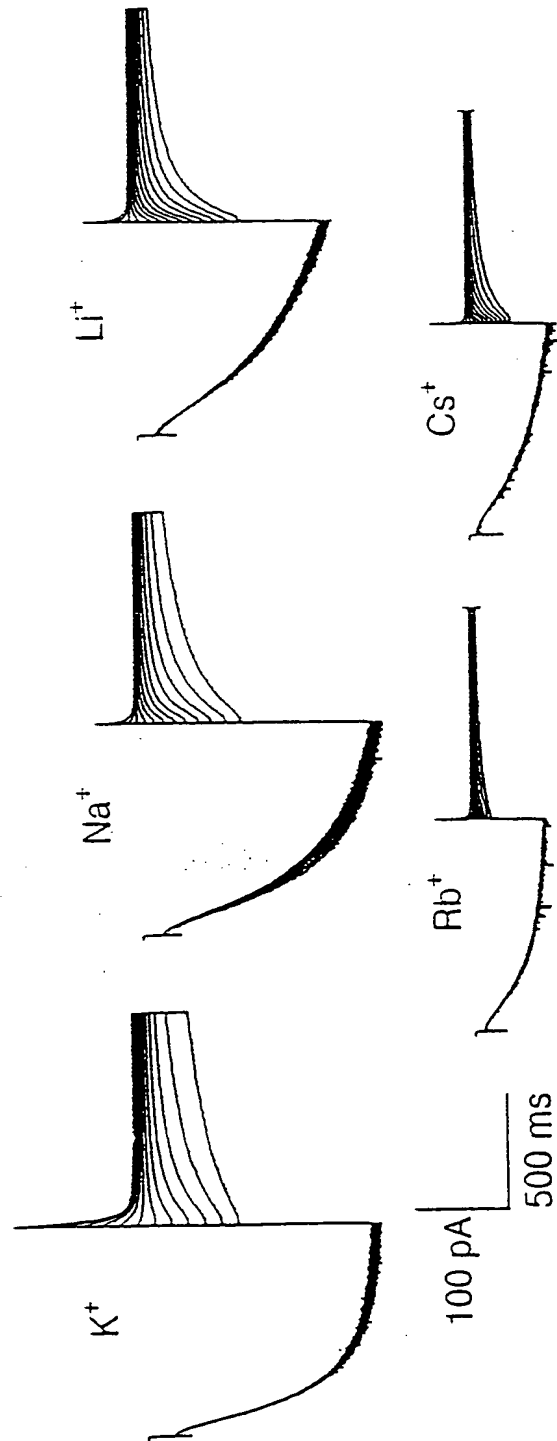


Fig. 4F

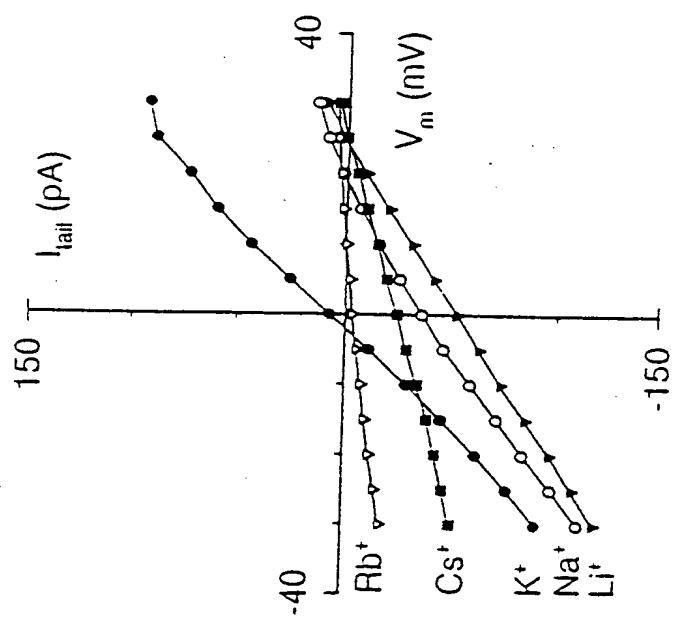


Fig. 4G

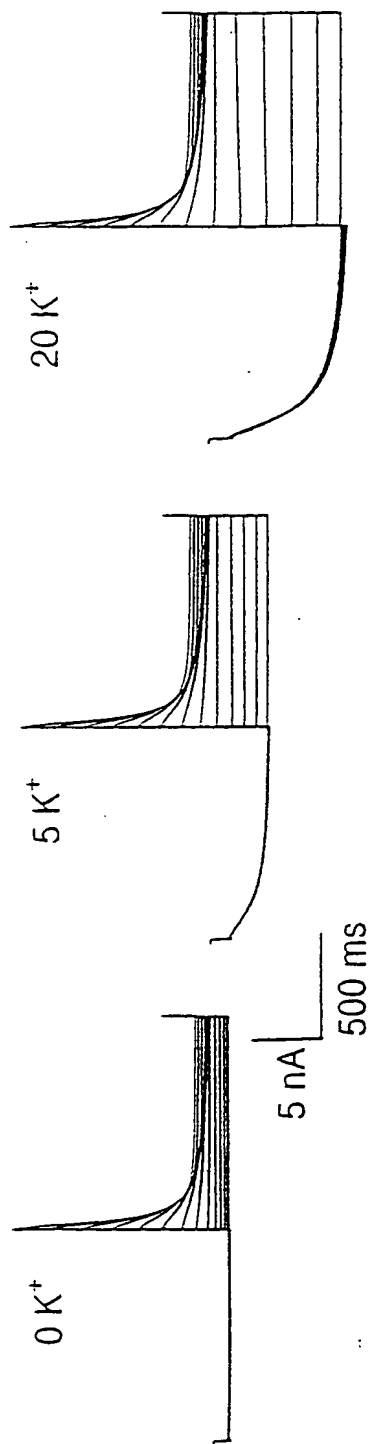


Fig. 4H

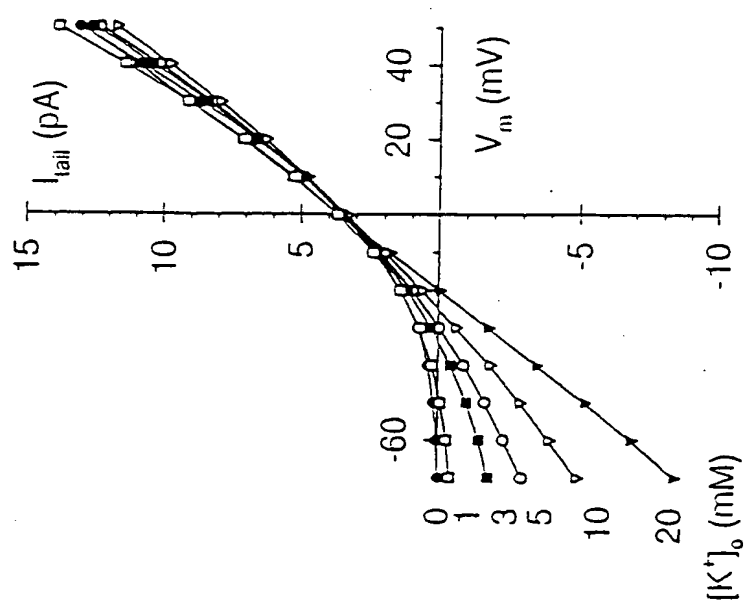




Fig. 5

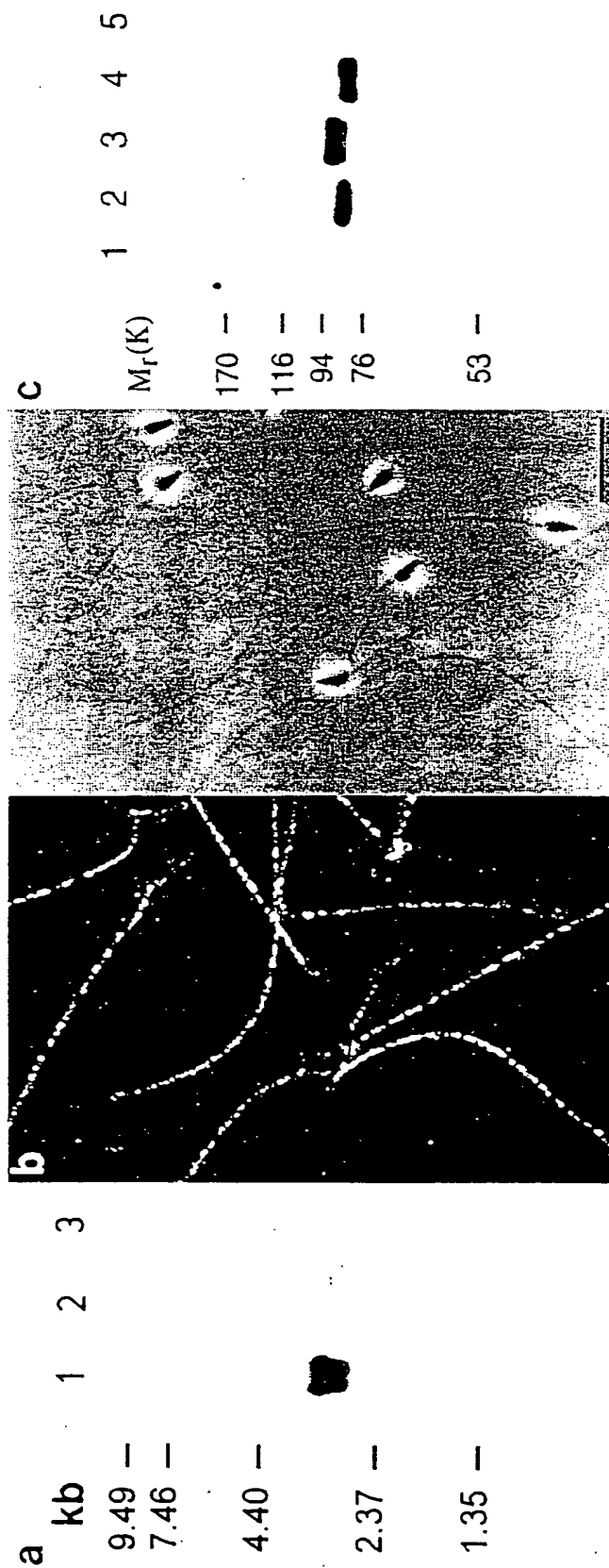


Fig. 6

